

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 10, 2004, 07:26:27 ; Search time 23 Seconds  
(without alignments)  
1335.541 Million cell updates/sec

Title: US-09-943-446a-6

Perfect score: 3169

Sequence: 1 MEAVHAPALALLCPVLS.....EASAPERPALLQEMETWM 595

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :  
1: Issued Patents AA:\*  
2: /cgn2\_6/prodata/2/iaa/5A\_COMB.pep:\*  
3: /cgn2\_6/prodata/2/iaa/5B\_COMB.pep:\*  
4: /cgn2\_6/prodata/2/iaa/5A\_COMB.pep:\*  
5: /cgn2\_6/prodata/2/iaa/5B\_COMB.pep:\*  
6: /cgn2\_6/prodata/2/iaa/backfill1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score  | Query Match | Length DB | ID | Description        |
|------------|--------|-------------|-----------|----|--------------------|
| 1          | 3020   | 95.3        | 593       | 2  | US-08-468-249A-21  |
| 2          | 2819   | 89.0        | 591       | 2  | US-08-468-249A-20  |
| 3          | 2444   | 77.1        | 585       | 2  | US-08-142-551B-125 |
| 4          | 2444   | 77.1        | 585       | 2  | US-08-468-249A-19  |
| 5          | 2440   | 77.0        | 585       | 1  | US-08-142-439A-6   |
| 6          | 2440   | 77.0        | 585       | 2  | US-08-468-249A-18  |
| 7          | 2286.5 | 72.2        | 515       | 2  | US-08-468-249A-17  |
| 8          | 1923.5 | 60.7        | 536       | 4  | US-09-449-632-2    |
| 9          | 1513.5 | 47.8        | 542       | 4  | US-09-449-632-4    |
| 10         | 1385   | 43.7        | 575       | 4  | US-09-449-632-5    |
| 11         | 1345.5 | 42.5        | 541       | 3  | US-08-468-011A-2   |
| 12         | 1345.5 | 42.5        | 541       | 4  | US-09-236-468A-2   |
| 13         | 1345.5 | 42.5        | 541       | 5  | PCT-US95-07085-2   |
| 14         | 994    | 31.4        | 207       | 4  | US-08-811-519-31   |
| 15         | 863    | 27.2        | 449       | 1  | US-08-142-439A-5   |
| 16         | 863    | 27.2        | 449       | 2  | US-08-869-477-5    |
| 17         | 855    | 27.0        | 1324      | 2  | US-08-811-897A-56  |
| 18         | 855    | 27.0        | 1324      | 4  | US-09-201-474-17   |
| 19         | 824    | 26.0        | 458       | 1  | US-08-112-817C-2   |
| 20         | 782.5  | 24.7        | 437       | 2  | US-08-538-816A-2   |
| 21         | 782.5  | 24.7        | 437       | 2  | US-09-076-651-2    |
| 22         | 782.5  | 24.7        | 437       | 4  | US-09-208-394-2    |
| 23         | 765.5  | 24.2        | 431       | 2  | US-08-538-816A-9   |
| 24         | 765.5  | 24.2        | 431       | 2  | US-09-076-651-9    |
| 25         | 765.5  | 24.2        | 431       | 4  | US-09-208-394-9    |
| 26         | 765.5  | 24.2        | 438       | 2  | US-08-538-816A-1   |
| 27         | 765.5  | 24.2        | 438       | 2  | US-09-076-651-1    |

|    |       |      |     |   |                   |                   |
|----|-------|------|-----|---|-------------------|-------------------|
| 28 | 765.5 | 24.2 | 438 | 4 | US-09-208-394-1   | Sequence 1, Appl  |
| 29 | 764.5 | 24.1 | 525 | 2 | US-08-811-897A-23 | Sequence 23, Appl |
| 30 | 764.5 | 24.1 | 525 | 2 | US-08-855-213-23  | Sequence 23, Appl |
| 31 | 764.5 | 24.1 | 525 | 4 | US-09-201-474-23  | Sequence 23, Appl |
| 32 | 754   | 23.8 | 448 | 2 | US-08-811-897A-22 | Sequence 22, Appl |
| 33 | 754   | 23.8 | 448 | 2 | US-08-855-213-22  | Sequence 22, Appl |
| 34 | 754   | 23.8 | 448 | 4 | US-09-201-474-22  | Sequence 22, Appl |
| 35 | 753.5 | 23.7 | 485 | 2 | US-08-811-897A-17 | Sequence 17, Appl |
| 36 | 752.5 | 23.7 | 485 | 2 | US-08-855-213-17  | Sequence 17, Appl |
| 37 | 752.5 | 23.7 | 485 | 4 | US-09-201-474-17  | Sequence 17, Appl |
| 38 | 752   | 23.7 | 552 | 2 | US-08-811-897A-27 | Sequence 27, Appl |
| 39 | 752   | 23.7 | 552 | 2 | US-08-855-213-27  | Sequence 27, Appl |
| 40 | 752   | 23.7 | 552 | 4 | US-09-201-474-27  | Sequence 27, Appl |
| 41 | 751.5 | 23.7 | 553 | 2 | US-08-811-897A-25 | Sequence 25, Appl |
| 42 | 751.5 | 23.7 | 553 | 2 | US-08-855-213-25  | Sequence 25, Appl |
| 43 | 751.5 | 23.7 | 553 | 4 | US-09-201-474-25  | Sequence 25, Appl |
| 44 | 750.5 | 23.7 | 467 | 2 | US-08-811-897A-19 | Sequence 19, Appl |
| 45 | 750.5 | 23.7 | 467 | 2 | US-08-855-213-19  | Sequence 19, Appl |

## ALIGNMENTS

RESULT 1  
US-08-468-249A-21  
Sequence 21, Application US/08468249A  
Patent No. 586148

### GENERAL INFORMATION:

APPLICANT: Segre et al., Gino V.  
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA  
TITLE OF INVENTION: ENCODING SAME  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESS: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,249A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/864,475  
FILING DATE: 06-APR-1992  
PRIOR APPLICATION NUMBER: US 07/681,702  
FILING DATE: 04-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 00786/071003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 593 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-468-249A-21

Query Match 95.3%; Score 3020; DB 2; Length 593;  
Best Local Similarity 95.2%; Pred. No. 4.6e-278;  
Matches 570; Conservative 5; Mismatches 14; Indels 10; Gaps 3;

QY 1 MGAARIAPGALILCCPYLSAVALVDADVMTKEBQIFILHRAOQOCCRLKEVLOPA 60  
 DB 1 MGAARIAPGALILCCPYLSAVALVDADVMTKEBQIFILHRAOQOCCRLKEVLOPA 60  
 QY 61 DIMESDKGMASTSGKPKKKAASKGLYPESEDEKVEYTGSRHGRCPCLPEMDHILCWL 120  
 DB 61 DIMESDKGMASTSGKPKKKAASKGLYPESEDEKVEYTGSRHGRCPCLPEMDHILCWL 120  
 QY 61 DIMESDKGMASTSGKPKKKAASKGLYPESEDEKVEYTGSRHGRCPCLPEMDHILCWL 120  
 DB 61 DIMESDKGMASTSGKPKKKAASKGLYPESEDEKVEYTGSRHGRCPCLPEMDHILCWL 120  
 QY 121 GAGEVAVAPCPDITVDENHGHAYRRCDNNGSMELVPGHNRWTANYSECVKLTNETRE 180  
 DB 121 GAGEVAVAPCPDITVDENHGHAYRRCDNNGSMELVPGHNRWTANYSECVKLTNETRE 180  
 QY 121 GAGEVAVAPCPDITVDENHGHAYRRCDNNGSMELVPGHNRWTANYSECVKLTNETRE 180  
 DB 121 GAGEVAVAPCPDITVDENHGHAYRRCDNNGSMELVPGHNRWTANYSECVKLTNETRE 180  
 QY 181 REVDRLGMITVGVSYSLASTVAVALILAYFRRLHCTRNIIHMLFLSFLRAVSIFFVK 240  
 DB 181 REVDRLGMITVGVSYSLASTVAVALILAYFRRLHCTRNIIHMLFLSFLRAVSIFFVK 240  
 QY 241 DAVISGATLDEAERLTHEELRAIAQAPPPATAAAGACRAVAVTFEFLATNTYWL 299  
 DB 241 DAVISGATLDEAERLTHEELRAIAQAPPPATAAAGACRAVAVTFEFLATNTYWL 299  
 QY 241 DAVISGATLDEAERLTHEELRAIAQAPPPATAAAGACRAVAVTFEFLATNTYWL 299  
 DB 241 DAVISGATLDEAERLTHEELRAIAQAPPPATAAAGACRAVAVTFEFLATNTYWL 299  
 QY 300 VEGYLHSLIFMAFSEKXYLMGFTVGMGLPAVFVAWVSVATLANTGCMDSGK 359  
 DB 300 VEGYLHSLIFMAFSEKXYLMGFTVGMGLPAVFVAWVSVATLANTGCMDSGK 359  
 QY 301 VEGYLHSLIFMAFSEKXYLMGFTVGMGLPAVFVAWVSVATLANTGCMDSGK 360  
 DB 301 VEGYLHSLIFMAFSEKXYLMGFTVGMGLPAVFVAWVSVATLANTGCMDSGK 360  
 QY 360 WIIQVPIIASIVNFIINIVRLATKRLTNAGRCCTROQYKRLKSTLVIMPLFGVH 419  
 DB 360 WIIQVPIIASIVNFIINIVRLATKRLTNAGRCCTROQYKRLKSTLVIMPLFGVH 419  
 QY 420 YIVFMATPYEVSGTLMOVQNHMELFNSFOGFVAIIYCFNGEVOAEIKKMSRWTLA 479  
 DB 420 YIVFMATPYEVSGTLMOVQNHMELFNSFOGFVAIIYCFNGEVOAEIKKMSRWTLA 479  
 QY 421 YIVFMATPYEVSGTLMOVQNHMELFNSFOGFVAIIYCFNGEVOAEIKKMSRWTLA 480  
 DB 421 YIVFMATPYEVSGTLMOVQNHMELFNSFOGFVAIIYCFNGEVOAEIKKMSRWTLA 480  
 QY 480 LDFKRAKASSSSSYSGPMVSHTSVTNVPRAAGLPLSPRLPAAAAATTATTNGHPPI 539  
 DB 480 LDFKRAKASSSSSYSGPMVSHTSVTNVPRAAGLPLSPRLPAAAAATTATTNGHPPI 539  
 QY 481 LDFKRAKASSSSSYSGPMVSHTSVTNVPRAAGLPLSPRLPAAAAATTATTNGHPPI 539  
 DB 481 LDFKRAKASSSSSYSGPMVSHTSVTNVPRAAGLPLSPRLPAAAAATTATTNGHPPI 539  
 QY 540 PGHTKPGAP---TLPATPPATAAPKDDGFLNGSCSGLDEEASAPRPPALLOEWEV 595  
 DB 540 PGHTKPGAP---TLPATPPATAAPKDDGFLNGSCSGLDEEASAPRPPALLOEWEV 595  
 QY 540 PGHTKPGAP---TLPATPPATAAPKDDGFLNGSCSGLDEEASAPRPPALLOEWEV 595  
 DB 540 PGHTKPGAP---TLPATPPATAAPKDDGFLNGSCSGLDEEASAPRPPALLOEWEV 595

RESULT 2  
 US-08-468-249A-20  
 Sequence 20, Application US/08468249A  
 Patent No. 5886148  
 GENERAL INFORMATION:  
 APPLICANT: Segre et al., Gino V.  
 TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA  
 TITLE OF INVENTION: ENCODING SAME  
 NUMBER OF SEQUENCES: 21  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Richardson P.C.  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/468,249A  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/864,475  
 FILING DATE: 06-APR-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/661,702  
 FILING DATE: 04-MAY-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fraser, Janis K.  
 REGISTRATION NUMBER: 34,819  
 REFERENCE/DOCKET NUMBER: 00786/071003  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/542-5070  
 TELEFAX: 617/542-8906  
 INFORMATION FOR SEQ ID NO: 20:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 591 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-468-249A-20  
 Query Match 89.0%; Score 2819; DB 2; Length 591;  
 Best Local Similarity 88.2%; Pred. No. 5.7e-259;  
 Matches 530; Conservative 21; Mismatches 34; Indels 16; Gaps 4;  
 QY 1 MGAARIAPGALILCCPYLSAVALVDADVMTKEBQIFILHRAOQOCCRLKEVLOPA 60  
 DB 1 MGAARIAPGALILCCPYLSAVALVDADVMTKEBQIFILHRAOQOCCRLKEVLOPA 60  
 QY 61 DIMESDKGMASTSGKPKKKAASKGLYPESEDEKVEYTGSRHGRCPCLPEMDHILCWL 120  
 DB 61 DIMESDKGMASTSGKPKKKAASKGLYPESEDEKVEYTGSRHGRCPCLPEMDHILCWL 120  
 QY 61 DIMESDKGMASTSGKPKKKAASKGLYPESEDEKVEYTGSRHGRCPCLPEMDHILCWL 120  
 DB 61 DIMESDKGMASTSGKPKKKAASKGLYPESEDEKVEYTGSRHGRCPCLPEMDHILCWL 120  
 QY 121 GAGEVAVAPCPDITVDENHGHAYRRCDNNGSMELVPGHNRWTANYSECVKLTNETRE 180  
 DB 121 GAGEVAVAPCPDITVDENHGHAYRRCDNNGSMELVPGHNRWTANYSECVKLTNETRE 180  
 QY 121 GAGEVAVAPCPDITVDENHGHAYRRCDNNGSMELVPGHNRWTANYSECVKLTNETRE 180  
 DB 121 GAGEVAVAPCPDITVDENHGHAYRRCDNNGSMELVPGHNRWTANYSECVKLTNETRE 180  
 QY 181 REVDRLGMITVGVSYSLASTVAVALILAYFRRLHCTRNIIHMLFLSFLRAVSIFFVK 240  
 DB 181 REVDRLGMITVGVSYSLASTVAVALILAYFRRLHCTRNIIHMLFLSFLRAVSIFFVK 240  
 QY 241 DAVISGATLDEAERLTHEELRAIAQAPPPATAAAGACRAVAVTFEFLATNTYWL 299  
 DB 241 DAVISGATLDEAERLTHEELRAIAQAPPPATAAAGACRAVAVTFEFLATNTYWL 299  
 QY 241 DAVISGATLDEAERLTHEELRAIAQAPPPATAAAGACRAVAVTFEFLATNTYWL 299  
 DB 241 DAVISGATLDEAERLTHEELRAIAQAPPPATAAAGACRAVAVTFEFLATNTYWL 299  
 QY 300 VEGYLHSLIFMAFSEKXYLMGFTVGMGLPAVFVAWVSVATLANTGCMDSGK 359  
 DB 300 VEGYLHSLIFMAFSEKXYLMGFTVGMGLPAVFVAWVSVATLANTGCMDSGK 359  
 QY 301 VEGYLHSLIFMAFSEKXYLMGFTVGMGLPAVFVAWVSVATLANTGCMDSGK 360  
 DB 301 VEGYLHSLIFMAFSEKXYLMGFTVGMGLPAVFVAWVSVATLANTGCMDSGK 360  
 QY 360 WIIQVPIIASIVNFIINIVRLATKRLTNAGRCCTROQYKRLKSTLVIMPLFGVH 419  
 DB 360 WIIQVPIIASIVNFIINIVRLATKRLTNAGRCCTROQYKRLKSTLVIMPLFGVH 419  
 QY 420 YIVFMATPYEVSGTLMOVQNHMELFNSFOGFVAIIYCFNGEVOAEIKKMSRWTLA 479  
 DB 420 YIVFMATPYEVSGTLMOVQNHMELFNSFOGFVAIIYCFNGEVOAEIKKMSRWTLA 479  
 QY 421 YIVFMATPYEVSGTLMOVQNHMELFNSFOGFVAIIYCFNGEVOAEIKKMSRWTLA 480  
 DB 421 YIVFMATPYEVSGTLMOVQNHMELFNSFOGFVAIIYCFNGEVOAEIKKMSRWTLA 480  
 QY 480 LDFKRAKASSSSSYSGPMVSHTSVTNVPRAAGLPLSPRLPAAAAATTATTNGHPPI 539  
 DB 480 LDFKRAKASSSSSYSGPMVSHTSVTNVPRAAGLPLSPRLPAAAAATTATTNGHPPI 539  
 QY 481 LDFKRAKASSSSSYSGPMVSHTSVTNVPRAAGLPLSPRLPAAAAATTATTNGHPPI 539  
 DB 481 LDFKRAKASSSSSYSGPMVSHTSVTNVPRAAGLPLSPRLPAAAAATTATTNGHPPI 539  
 QY 540 PGHTKPGAP---TLPATPPATAAPKDDGFLNGSCSGLDEEASAPRPPALLOEWEV 594  
 DB 540 PGHTKPGAP---TLPATPPATAAPKDDGFLNGSCSGLDEEASAPRPPALLOEWEV 594  
 QY 540 PGHTKPGAP---TLPATPPATAAPKDDGFLNGSCSGLDEEASAPRPPALLOEWEV 594  
 DB 540 PGHTKPGAP---TLPATPPATAAPKDDGFLNGSCSGLDEEASAPRPPALLOEWEV 594

RESULT 3  
 US-08-142-551B-125  
 Sequence 125, Application US/08142551B  
 Patent No. 5814603  
 GENERAL INFORMATION:  
 APPLICANT: Oldenburg, Kevin R.  
 TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND  
 TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME  
 NUMBER OF SEQUENCES: 132

405 May